

seq id.ST25
SEQUENCE LISTING

<110> Mirus Corporation
Wong, So
Wakefield, Darren
Sokoloff, Alex
Monahan, Sean
Sebestyen, Magdolna
Wolff, Jon
Higgs, Lori

<120> A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO

<130> Mirus.014.06

<160> 36

<170> PatentIn version 3.1

<210> 1

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<212> PRT

<213> Bacteriophage T7

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1 5 10 15

Arg Gly Ser His Met Ala Asn Val Ile Lys Thr Val Leu Thr Tyr Gln
20 25 30

Leu Asp Gly Ser Asn Arg Asp Phe Asn Ile Pro Phe Glu Tyr Leu Ala
35 40 45

Arg Lys Phe Val Val Val Thr Leu Ile Gly Val Asp Arg Lys Val Leu
50 55 60

Thr Ile Asn Thr Asp Tyr Arg Phe Ala Thr Arg Thr Thr Ile Ser Leu
65 70 75 80

Thr Lys Ala Trp Gly Pro Ala Asp Gly Tyr Thr Thr Ile Glu Leu Arg
85 90 95

Arg Val Thr Ser Thr Thr Asp Arg Leu Val Asp Phe Thr Asp Gly Ser
100 105 110

Ile Leu Arg Ala Tyr Asp Leu Asn Val Ala Gln Ile Gln Thr Met His
115 120 125

Val Ala Glu Glu Ala Arg Asp Leu Thr Thr Asp Thr Ile Gly Val Asn
130 135 140

Asn Asp Gly His Leu Asp Ala Arg Gly Arg Arg Ile Val Asn Leu Ala
145 150 155 160

Asn Ala Val Asp Asp Arg Asp Ala Val Pro Phe Gly Gln Leu Lys Thr
165 170 175

Met Asn Gln Asn Ser Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg
180 185 190

Asn Glu Ala Glu Thr Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu
195 200 205

Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys
210 215 220

Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr
225 230 235 240

Ala Thr Ser Ala Gly Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val
245 250 255

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Asn Ala Glu Asn Ser Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala
260 265 270

Glu Gln Gln Ala Asp Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn
275 280 285

Tyr Asn Gly Leu Ala Gly Ala Ile Asp Lys Val Asp Gly Thr Asn Val
290 295 300

Tyr Trp Lys Gly Asn Ile His Ala Asn Gly Arg Leu Tyr Met Thr Thr
305 310 315 320

Asn Gly Phe Asp Cys Gly Gln Tyr Gln Gln Phe Phe Gly Gly Val Thr
325 330 335

Asn Arg Tyr Ser Val Met Glu Trp Gly Asp Glu Asn Gly Trp Leu Met
340 345 350

Tyr Val Gln Arg Arg Glu Trp Thr Thr Ala Ile Gly Gly Asn Ile Gln
355 360 365

Leu Val Val Asn Gly Gln Ile Ile Thr Gln Gly Gly Ala Met Thr Gly
370 375 380

Gln Leu Lys Leu Gln Asn Gly His Val Leu Gln Leu Glu Ser Ala Ser
385 390 395 400

Asp Lys Ala His Tyr Ile Leu Ser Lys Asp Gly Asn Arg Asn Asn Trp
405 410 415

Tyr Ile Gly Arg Gly Ser Asp Asn Asn Asn Asp Cys Thr Phe His Ser
420 425 430

Tyr Val His Gly Thr Thr Leu Thr Leu Lys Gln Asp Tyr Ala Val Val
435 440 445

Asn Lys His Phe His Val Gly Gln Ala Val Val Ala Thr Asp Gly Asn
450 455 460

Ile Gln Gly Thr Lys Trp Gly Gly Lys Trp Leu Asp Ala Tyr Leu Arg
465 470 475 480

Asp Ser Phe Val Ala Lys Ser Lys Ala Trp Thr Gln Val Trp Ser Gly
485 490 495

Ser Ala Gly Gly Gly Val Ser Val Thr Val Ser Gln Asp Leu Arg Phe
500 505 510

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Arg Asn Ile Trp Ile Lys Cys Ala Asn Asn Ser Trp Asn Phe Phe Arg
515 520 525

Thr Gly Pro Asp Gly Ile Tyr Phe Ile Ala Ser Asp Gly Gly Trp Leu
530 535 540

Arg Phe Gln Ile His Ser Asn Gly Leu Gly Phe Lys Asn Ile Ala Asp
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<400> 5

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1 5 10 15

Arg Gly Ser His Pro Phe Gly Gln Leu Lys Thr Met Asn Gln Asn Ser
20 25 30

Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg Asn Glu Ala Glu Thr
35 40 45

Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu Ser Ser Thr Asn Ala
50 55 60

Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe Arg Asp Glu
65 70 75 80

Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr Ala Thr Ser Ala Gly
85 90 95

Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val Asn Ala Glu Asn Ser
100 105 110

Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala Glu Gln Gln Ala Asp
115 120 125

Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn Tyr Asn Gly Leu Ala
130 135 140

Gly Ala Ile Asp Lys Val Asp Gly Thr Asn Val Tyr Trp Lys Gly Asn
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<213> Bacteriophage T7

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Arg Gly Ser His Met Ala Asn Val Ile Lys Thr Val Leu Thr Tyr Gln
20 25 30

Leu Asp Gly Ser Asn Arg Asp Phe Asn Ile Pro Phe Glu Tyr Leu Ala
35 40 45

Arg Lys Phe Val Val Val Thr Leu Ile Gly Val Asp Arg Lys Val Leu
50 55 60

Thr Ile Asn Thr Asp Tyr Arg Phe Ala Thr Arg Thr Thr Ile Ser Leu
65 70 75 80

Thr Lys Ala Trp Gly Pro Ala Asp Gly Tyr Thr Thr Ile Glu Leu Arg
85 90 95

Arg Val Thr Ser Thr Asp Arg Leu Val Asp Phe Thr Asp Gly Ser
100 105 110

Ile Leu Arg Ala Tyr Asp Leu Asn Val Ala Gln Ile Gln Thr Met His
115 120 125

Val Ala Glu Glu Ala Arg Asp Leu Thr Thr Asp Thr Ile Gly Val Asn
130 135 140

Asn Asp Gly His Leu Asp Ala Arg Gly Arg Arg Ile Val Asn Leu Ala
145 150 155 160

Asn Ala Val Asp Asp Arg Asp Ala Val Pro Phe Gly Gln Leu Lys Thr
165 170 175

Met Asn Gln Asn Ser Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg
180 185 190

Asn Glu Ala Glu Thr Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu
195 200 205

Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys
210 215 220

seq id.ST25

Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr
225 230 235 240

Ala Thr Ser Ala Gly Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val
245 250 255

Asn Ala Glu Asn Ser Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala
260 265 270

Glu Gln Gln Ala Asp Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn
275 280 285

Tyr Asn Gly Leu Ala Gly Ala Ile Asp Lys Val Asp Gly Thr Asn Val
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Tyr Trp Lys Gly Asn
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<212> PRT

<213> Bacteriophage T7

<400> 7

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
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Arg Gly Ser His Pro Phe Gly Gln Leu Lys Thr Met Asn Gln Asn Ser
20 25 30

Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg Asn Glu Ala Glu Thr
35 40 45

Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu Ser Ser Thr Asn Ala
50 55 60

Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe Arg Asp Glu
65 70 75 80

Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr Ala Thr Ser Ala Gly
85 90 95

Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val Asn Ala Glu Asn Ser
100 105 110

Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala Glu Gln Gln Ala Asp
115 120 125

seq id.ST25

Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn Tyr Asn Gly Leu Ala
130 135 140

Gly Ala Ile Asp Lys Val Asp Gly Thr Asn Val Tyr Trp Lys Gly Asn
145 150 155 160

Ile His Ala Asn Gly Arg Leu Tyr Met Thr Thr Asn Gly Phe Asp Cys
165 170 175

Gly Gln Tyr Gln Gln Phe Phe Gly Gly Val Thr Asn Arg Tyr Ser Val
180 185 190

Met Glu Trp Gly Asp Glu Asn Gly Trp Leu Met Tyr Val Gln Arg Arg
195 200 205

Glu Trp Thr Thr Ala Ile Gly Gly Asn Ile Gln Leu Val Val Asn Gly
210 215 220

Gln Ile Ile Thr Gln Gly Gly Ala Met Thr Gly Gln Leu Lys Leu Gln
225 230 235 240

Asn Gly His Val Leu Gln Leu Glu Ser Ala Ser Asp Lys Ala His Tyr
245 250 255

Ile Leu Ser Lys Asp Gly Asn Arg Asn Asn Trp Tyr Ile Gly Arg Gly
260 265 270

Ser Asp Asn Asn Asn Asp Cys Thr Phe His Ser Tyr Val His Gly Thr
275 280 285

Thr Leu Thr Leu Lys Gln Asp Tyr Ala Val Val Asn Lys His Phe His
290 295 300

Val Gly Gln Ala Val Val Ala Thr Asp Gly Asn Ile Gln Gly Thr Lys
305 310 315 320

Trp Gly Gly Lys Trp Leu Asp Ala Tyr Leu Arg Asp Ser Phe Val Ala
325 330 335

Lys Ser Lys Ala Trp Thr Gln Val Trp Ser Gly Ser Ala Gly Gly Gly
340 345 350

Val Ser Val Thr Val Ser Gln Asp Leu Arg Phe Arg Asn Ile Trp Ile
355 360 365

Lys Cys Ala Asn Asn Ser Trp Asn Phe Phe Arg Thr Gly Pro Asp Gly

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Asn Ala Ile Met Val Glu Asn Glu 420		
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Glu Thr Lys Gly Phe Arg Asp Glu Ala Arg Arg Phe Lys Asn Thr Ala
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Gly

<210> 15

<211> 33

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<213> Bacteriophage T7

<400> 15

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Lys Asp
1 5 10 15

Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala
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Gly

<210> 16

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<213> Bacteriophage T7

<400> 16

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp
1 5 10 15

Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala
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Gly Gln Tyr Ala Thr Ser Ala Gly
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<210> 17
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<213> Bacteriophage T7

<400> 17

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1 5 10 15

Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asp Glu Ala
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Gly

<210> 18
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<213> Bacteriophage T7

<400> 18

Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe
1 5 10 15

Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
20 25

<210> 19
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<213> Bacteriophage T7

<400> 19

Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly
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Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
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<210> 20
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<213> Bacteriophage T7

<400> 20

Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys
1 5 10 15

Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
20 25 30

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<210> 21
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<213> Bacteriophage T7

<400> 21

Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr
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Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
20 25 30

<210> 22
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<400> 22

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp
1 5 10 15

Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala
20 25 30

Gly

<210> 23
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<212> PRT
<213> Bacteriophage T7

<400> 23

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp
1 5 10 15

Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala
20 25 30

Gly

<210> 24
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<400> 24

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp
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Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe
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Glu Thr Lys Gly Phe Arg Asp Glu Ala Glu Arg Phe Lys Asn Thr Ala
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Gly

<210> 26
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<400> 26

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Glu Thr Lys Gly Phe Arg Asp Glu Ala Arg Arg Phe Arg Asn Thr Ala
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Gly

<210> 27
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<212> PRT
<213> Bacteriophage T7

<400> 27

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Arg Gln Trp Arg Asp
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Glu Thr Arg Gly Phe Arg Asp Glu Ala Arg Arg Phe Lys Asn Thr Ala
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Gly

seq id.ST25

<210> 28

<211> 25

<212> PRT

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<400> 28

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp
1 5 10 15

Glu Thr Lys Gly Phe Arg Asp Glu Ala
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<210> 29

<211> 25

<212> PRT

<213> Bacteriophage T7

<400> 29

Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys
1 5 10 15

Gly Phe Arg Asp Glu Ala Lys Arg Phe
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<210> 30

<211> 28

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<213> Bacteriophage T7

<400> 30

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp
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Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe
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<210> 31

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<213> Bacteriophage T7

<400> 31

Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
1 5 10 15

<210> 32

<211> 22

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<400> 32

Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg
1 5 10 15 seq id.ST25

Phe Lys Asn Thr Ala Gly
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<210> 33
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<212> PRT
<213> Bacteriophage T7

<400> 33

Leu Lys Thr Met Asn Gln Asn Ser Trp Gln Ala Arg Asn Glu Ala Leu
1 5 10 15

Gln Phe Arg Asn Glu Ala Glu Thr Gly Arg Asn Gln Ala
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<210> 34
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<213> Bacteriophage T7

<400> 34

Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe Arg Asp
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Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr Ala Thr Ser Ala
20 25 30

Gly

<210> 35
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<212> PRT
<213> Bacteriophage T7

<400> 35

Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe Arg
1 5 10 15

Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
20 25

<210> 36
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<213> Bacteriophage T7

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seq id.ST25

Lys Asn Glu Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp
1 5 10 15

Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala
20 25 30

Gly